

SEQUENCE LISTING

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(1) GENERAL INFORMATION

(i) APPLICANT: Summers, Neena
McWherter, Charles
Feng, Yiqing

(ii) TITLE OF THE INVENTION: Novel Erythropoietin Receptor Agonists

(iii) NUMBER OF SEQUENCES: 134

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: G. D. Searle & Co.
(B) STREET: P.O. Box 5110
(C) CITY: Chicago
(D) STATE: IL
(E) COUNTRY: U. S. A.
(F) ZIP: 60680

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 21-OCT-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/034,044
(B) FILING DATE: 25-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bennett, Dennis A
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(C) REFERENCE/DOCKET NUMBER: 2991/1

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile
1				5					10				15		
Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu
				20				25				30			
Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser
				35				40				45			
Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro
				50				55				60			
Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg
				65				70				75			80
Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile
				85				90				95			
Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala
				100				105				110			
Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly

115	120	125
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly		
130	135	140
Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu		
145	150	155
Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu		
165	170	

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr			
1	5	10	15
Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val			
20	25	30	
Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Ser Glu			
35	40	45	
Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp			
50	55	60	
Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser			
65	70	75	80
Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser			
85	90	95	
Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp			
100	105	110	
Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys			
115	120	125	
Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly			
130	135	140	
Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg			
145	150	155	160
Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn			
165	170		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val			
1	5	10	15
Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly			
20	25	30	
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Ser Glu Ala			
35	40	45	
Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu			
50	55	60	
Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu			
65	70	75	80
Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro			
85	90	95	
Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr			
100	105	110	
Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu			
115	120	125	
Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly			
130	135	140	
Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr			
145	150	155	160
Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile			
165	170		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp
1				5					10					15	
Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln
				20				25					30		
Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu
		35				40					45				
Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu
	50				55					60					
Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr
	65				70				75				80		
Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp
				85				90				95			
Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg
				100				105				110			
Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu
		115				120				125					
Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly	Gly	Ser	Ala
	130				135					140					
Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu
	145				150				155				160		
Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr							
					165			170							

(2) INFORMATION FOR SEO ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr
1				5				10					15		
Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala
			20				25						30		
Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg
	35				40					45					
Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln
	50				55					60					
Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu
	65				70					75					80
Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala
				85				90					95		
Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys
				100				105					110		
Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr
			115				120				125				
Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly	Gly	Ser	Ala	Pro
				130			135				140				
Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu
	145				150					155					160
Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly						
				165					170						

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys
1				5					10					15	
Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val
			20					25						30	
Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly
			35				40			45					
Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu
					50		55			60					
His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu
					65		70			75					80
Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala
					85			90					95		
Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu
					100			105					110		
Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr
					115			120			125				
Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly	Gly	Ser	Ala	Pro	Pro
					130		135			140					
Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala
					145		150			155					160
Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys						
					165			170							

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val

1	5	10	15
Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu			
20	25	30	
Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln			
35	40	45	
Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His			
50	55	60	
Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg			
65	70	75	80
Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser			
85	90	95	
Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe			
100	105	110	
Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly			
115	120	125	
Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg			
130	135	140	
Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys			
145	150	155	160
Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala			
165	170		

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn			
1	5	10	15
Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val			
20	25	30	
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala			
35	40	45	
Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val			
50	55	60	
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala			
65	70	75	80
Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala			
85	90	95	
Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg			
100	105	110	
Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu			
115	120	125	
Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu			
130	135	140	
Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu			
145	150	155	160
Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu			
165	170		

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe			
1	5	10	15
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp			
20	25	30	
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu			
35	40	45	
Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp			
50	55	60	

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
 65 70 75 80
 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
 85 90 95
 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 100 105 110
 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
 115 120 125
 Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile
 130 135 140
 Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala
 145 150 155 160
 Glu Asn Ile Thr Thr Gly Cys Ala Glu His
 165 170

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr
 1 5 10 15
 Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln
 20 25 30
 Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
 35 40 45
 Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys
 50 55 60
 Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
 65 70 75 80
 Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro
 85 90 95
 Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr
 100 105 110
 Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys
 115 120 125
 Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys
 130 135 140
 Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu
 145 150 155 160
 Asn Ile Thr Thr Gly Cys Ala Glu His Cys
 165 170

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala
 1 5 10 15
 Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly
 20 25 30
 Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val
 35 40 45
 Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala
 50 55 60
 Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala
 65 70 75 80
 Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu
 85 90 95
 Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser
 100 105 110
 Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg

115	120	125
Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp		
130	135	140
Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn		
145	150	155
Ile Thr Thr Gly Cys Ala Glu His Cys Ser		
165	170	

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp			
1	5	10	15
Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu			
20	25	30	
Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn			
35	40	45	
Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val			
50	55	60	
Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln			
65	70	75	80
Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg			
85	90	95	
Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn			
100	105	110	
Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr			
115	120	125	
Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser			
130	135	140	
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile			
145	150	155	160
Thr Thr Gly Cys Ala Glu His Cys Ser Leu			
165	170		

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys			
1	5	10	15
Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala			
20	25	30	
Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser			
35	40	45	
Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser			
50	55	60	
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys			
65	70	75	80
Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr			
85	90	95	
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe			
100	105	110	
Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly			
115	120	125	
Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg			
130	135	140	
Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr			
145	150	155	160
Thr Gly Cys Ala Glu His Cys Ser Leu Asn			
165	170		

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg
1							5		10				15		
Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu
							20		25				30		
Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser
							35		40				45		
Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly
							50		55				60		
Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu
							65		70				80		
Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile
							85		90				95		
Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu
							100		105				110		
Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp
							115		120				125		
Arg	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	
							130		135				140		
Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr
							145		150				155		
Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu						160
							165								170

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met
1						5		10				15			
Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu
							20		25				30		
Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln
							35		40				45		
Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu
							50		55				60		
Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala
							65		70				80		
Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr
							85		90				95		
Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg
							100		105				110		
Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg
							115		120				125		
Gly	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu
							130		135				140		
Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly
							145		150				155		
Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn						160
							165								170

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val
1				5					10				15		
Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu
				20				25				30			
Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp
				35				40			45				
Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser
				50				55			60				
Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser
				65				70			75			80	
Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp
				85					90			95			
Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys
				100				105			110				
Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly
				115				120			125				
Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg
				130				135			140				
Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala
				145				150			155			160	
Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr						
				165				170							

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly
1				5					10			15			
Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala
				20				25			30				
Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu
				35				40			45				
Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu
				50				55			60				
Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro
				65				70			75			80	
Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr
				85					90			95			
Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu
				100				105			110				
Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly	Gly
				115				120			125				
Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr
				130				135			140				
Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu
				145				150			155			160	
His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val						
				165				170							

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln

DEPARTMENT OF ENERGY

1 5 10 15
 Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val
 20 25 30
 Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
 35 40 45
 Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr
 50 55 60
 Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro
 65 70 75 80
 Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
 85 90 95
 Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys
 100 105 110
 Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser
 115 120 125
 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
 130 135 140
 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
 145 150 155 160
 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro
 165 170

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
 1 5 10 15
 Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser
 20 25 30
 Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
 35 40 45
 Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys
 50 55 60
 Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
 65 70 75 80
 Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe
 85 90 95
 Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly
 100 105 110
 Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg
 115 120 125
 Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr
 130 135 140
 Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro
 145 150 155 160
 Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 1 5 10 15
 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 20 25 30
 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 35 40 45
 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 50 55 60

DRAFT - NOT FOR CITATION

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 65 70 75 80
 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 85 90 95
 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 100 105 110
 Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val
 115 120 125
 Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
 130 135 140
 Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp
 145 150 155 160
 Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 165 170

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu
 1 5 10 15
 Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln
 20 25 30
 Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu
 35 40 45
 Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala
 50 55 60
 Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr
 65 70 75 80
 Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
 85 90 95
 Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
 100 105 110
 Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu
 115 120 125
 Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly
 130 135 140
 Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr
 145 150 155 160
 Lys Val Asn Phe Tyr Ala Trp Lys Arg Met
 165 170

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser
 1 5 10 15
 Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro
 20 25 30
 Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg
 35 40 45
 Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile
 50 55 60
 Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
 65 70 75 80
 Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
 85 90 95
 Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly
 100 105 110
 Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu

115		120		125											
Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys
130						135					140				
Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys
145					150					155					160
Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu						
					165				170						

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu
1				5				10					15		
His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu
			20					25					30		
Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala
			35				40				45				
Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu
			50			55					60				
Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr
			65			70				75					80
Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly	Gly	Ser	Ala	Pro	Pro
				85				90					95		
Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala
				100				105					110		
Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu
				115				120				125			
Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp
				130			135				140				
Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu
			145			150				155					160
Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly						
				165				170							

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His
 1 5 10 15
 Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
 20 25 30
 Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser
 35 40 45
 Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe
 50 55 60
 Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly
 65 70 75 80
 Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg
 85 90 95
 Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys
 100 105 110
 Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn
 115 120 125
 Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys
 130 135 140
 Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
 145 150 155 160
 Leu Leu Ser Glu Ala Val Leu Arg Gly Gln
 165 170

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val
1				5					10					15	
Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Arg	Ala	
					20				25					30	
Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala
						35		40				45			
Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg
						55					60				
Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu
					65		70			75					80
Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu
					85				90					95	
Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu
					100			105						110	
Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu
						115		120				125			
Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg
						130		135			140				
Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu
					145		150			155					160
Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala						
					165				170						

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp
1				5				10						15	
Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu
				20				25						30	
Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala
				35				40					45		
Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val
				50				55				60			
Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala
				65				70				75			80
Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	
				85				90					95		
Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala
				100				105					110		
Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn
				115				120				125			
Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met
				130				135				140			
Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu
				145				150				155			160
Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu						
				165				170							

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys
1				5					10				15		
Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly
			20					25				30			
Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro
	35					40				45					
Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr
	50					55			60						
Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys
	65					70			75			80			
Arg	Thr	Gly	Asp	Arg	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	
	85						90				95				
Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu
	100					105			110			110			
Asn	Ile	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	
	115					120			125						
Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu
	130				135				140						
Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser
	145					150			155			160			
Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu						
	165					170									

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala
1				5				10				15			
Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala
			20				25			30					
Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu
	35					40			45						
Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser
	50					55			60						
Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg
	65					70			75			80			
Thr	Gly	Asp	Arg	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	
	85						90			95					
Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn
	100					105			110			110			
Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Ile	Thr	
	115					120			125						
Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val
	130					135			140						
Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu
	145					150			155			160			
Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val						
	165					170									

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val

1	5	10	15
Ser	Gly	Leu	Arg
20	25	30	
Lys	Glu	Ala	Ile
35	40	45	
Thr	Ile	Ser	Pro
50	55	60	
Phe	Arg	Lys	Leu
65	70	75	80
Gly	Asp	Gly	Gly
85	90	95	
Arg	Val	Leu	Glu
100	105	110	
Thr	Thr	Gly	Cys
115	120	125	
Pro	Asp	Thr	Lys
130	135	140	
Gln	Gln	Ala	Val
145	150	155	160
Val	Leu	Arg	Gly
165	170		
Gln	Ala	Leu	Leu
		Val	Asn

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser
1	5	10	15												
Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys
20	25	30													
Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr
35	40	45													
Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe
50	55	60													
Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly
65	70	75	80												
Asp	Arg	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	
85	90	95													
Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr
100	105	110													
Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro
115	120	125													
Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln
130	135	140													
Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val
145	150	155	160												
Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser						
165	170														

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly
1	5	10	15												
Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu
20	25	30													
Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile
35	40	45													
Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu
50	55	60													

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Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 65 70 75 80
 Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val
 85 90 95
 Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
 100 105 110
 Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp
 115 120 125
 Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln
 130 135 140
 Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
 145 150 155 160
 Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 165 170

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu
 1 5 10 15
 Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala
 20 25 30
 Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr
 35 40 45
 Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
 50 55 60
 Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
 65 70 75 80
 Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu
 85 90 95
 Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly
 100 105 110
 Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr
 115 120 125
 Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
 130 135 140
 Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg
 145 150 155 160
 Gly Gln Ala Leu Leu Val Asn Ser Ser Gln
 165 170

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg
 1 5 10 15
 Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile
 20 25 30
 Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
 35 40 45
 Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
 50 55 60
 Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly
 65 70 75 80
 Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu
 85 90 95
 Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys
 100 105 110
 Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys

115	120	125
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val		
130	135	140
Glu Val Trp Gln Gly Leu Ala Leu Ser Glu Ala Val Leu Arg Gly		
145	150	155
Gln Ala Leu Leu Val Asn Ser Ser Gln Pro		160
165	170	

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser			
1	5	10	15
Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser			
20	25	30	
Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp			
35	40	45	
Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys			
50	55	60	
Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly			
65	70	75	80
Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg			
85	90	95	
Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala			
100	105	110	
Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val			
115	120	125	
Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu			
130	135	140	
Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln			
145	150	155	160
Ala Leu Leu Val Asn Ser Ser Gln Pro Trp			
165	170		

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala			
1	5	10	15
Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys			
20	25	30	
Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr			
35	40	45	
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro			
50	55	60	
Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu			
65	70	75	80
Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser			
85	90	95	
Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala			
100	105	110	
Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly			
115	120	125	
Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val			
130	135	140	
Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala			
145	150	155	160
Val Ser Gly Leu Arg Ser Leu Thr Thr Leu			
165	170		

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala
1															15
Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu
															30
Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr
															45
Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly	Ser	Ala	Pro	Pro	
															50
Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala
															65
Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu
															85
Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp
															100
Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu
															115
Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn
															130
Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val
															145
Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu						
															165
															170

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser
1															15
Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe
															20
Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly
															35
Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly	Ser	Ala	Pro	Pro	Arg	
															50
Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys
															65
Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn
															85
Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys
															100
Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala
															115
Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser
															130
Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser
															145
Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg						
															165
															170

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala
 1 5 10 15
 Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg
 20 25 30
 Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu
 35 40 45
 Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu
 50 55 60
 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Glu Ala Lys Glu
 65 70 75 80
 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 85 90 95
 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 100 105 110
 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 115 120 125
 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 130 135 140
 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 145 150 155 160
 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala
 165 170

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
 1 5 10 15
 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 20 25 30
 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
 35 40 45
 Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile
 50 55 60
 Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala
 65 70 75 80
 Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
 85 90 95
 Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met
 100 105 110
 Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu
 115 120 125
 Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln
 130 135 140
 Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu
 145 150 155 160
 Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro

1	5	10	15
Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr			
20	25	30	
Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys			
35	40	45	
Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys			
50	55	60	
Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu			
65	70	75	80
Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile			
85	90	95	
Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu			
100	105	110	
Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser			
115	120	125	
Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro			
130	135	140	
Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg			
145	150	155	160
Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly			
165	170		

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu			
1	5	10	15
Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser			
20	25	30	
Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg			
35	40	45	
Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp			
50	55	60	
Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn			
65	70	75	80
Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr			
85	90	95	
Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val			
100	105	110	
Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu			
115	120	125	
Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp			
130	135	140	
Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser			
145	150	155	160
Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala			
165	170		

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg			
1	5	10	15
Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn			
20	25	30	
Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr			
35	40	45	
Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser			
50	55	60	

Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
 65 70 75 80
 Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
 85 90 95
 Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
 100 105 110
 Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
 115 120 125
 Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu
 130 135 140
 Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
 145 150 155 160
 Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln
 165 170

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
 1 5 10 15
 Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe
 20 25 30
 Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly
 35 40 45
 Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg
 50 55 60
 Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr
 65 70 75 80
 Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro
 85 90 95
 Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln
 100 105 110
 Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val
 115 120 125
 Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
 130 135 140
 Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr
 145 150 155 160
 Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 1 5 10 15
 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 20 25 30
 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 35 40 45
 Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val
 50 55 60
 Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
 65 70 75 80
 Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp
 85 90 95
 Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln
 100 105 110
 Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu

115	120	125
Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu		
130	135	140
Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr		
145	150	155
Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu		160
165	170	

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr			
1	5	10	15
Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg			
20	25	30	
Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg			
35	40	45	
Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu			
50	55	60	
Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Asn Ile Thr Thr Gly			
65	70	75	80
Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr			
85	90	95	
Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala			
100	105	110	
Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg			
115	120	125	
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln			
130	135	140	
Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu			
145	150	155	160
Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala			
165	170		

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala			
1	5	10	15
Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly			
20	25	30	
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly			
35	40	45	
Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu			
50	55	60	
Arg Tyr Leu Leu Glu Ala Lys Glu Ala Asn Ile Thr Thr Gly Cys			
65	70	75	80
Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys			
85	90	95	
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val			
100	105	110	
Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly			
115	120	125	
Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu			
130	135	140	
His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu			
145	150	155	160
Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile			
165	170		

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp
 1          5          10          15
Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys
 20         25          30
Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly
 35         40          45
Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
 50         55          60
Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
 65         70          75          80
Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val
 85         90          95
Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu
100        105         110
Val Trp Gln Gly Leu Ala Leu Ser Glu Ala Val Leu Arg Gly Gln
115        120         125
Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His
130        135         140
Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
145        150         155         160
Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
165        170

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(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr
 1          5          10          15
Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu
 20         25          30
Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly
 35         40          45
Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
 50         55          60
Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu
 65         70          75          80
His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn
 85         90          95
Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val
100        105         110
Trp Gln Gly Leu Ala Leu Ser Glu Ala Val Leu Arg Gly Gln Ala
115        120         125
Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val
130        135         140
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala
145        150         155         160
Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro
165        170

```

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
 1 5 10 15
 Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys
 20 25 30
 Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser
 35 40 45
 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
 50 55 60
 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
 65 70 75 80
 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
 85 90 95
 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
 100 105 110
 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
 115 120 125
 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
 130 135 140
 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
 145 150 155 160
 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro
 165 170

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg
 1 5 10 15
 Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu
 20 25 30
 Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala
 35 40 45
 Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu
 50 55 60
 Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys
 65 70 75 80
 Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr
 85 90 95
 Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln
 100 105 110
 Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
 115 120 125
 Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys
 130 135 140
 Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
 145 150 155 160
 Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp
 165 170

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys

26126574966600

1	5	10	15
Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr			
20	25	30	
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro			
35	40	45	
Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu			
50	55	60	
Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser			
65	70	75	80
Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala			
85	90	95	
Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly			
100	105	110	
Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val			
115	120	125	
Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala			
130	135	140	
Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala			
145	150	155	160
Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala			
165	170		

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu			
1	5	10	15
Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr			
20	25	30	
Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro			
35	40	45	
Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala			
50	55	60	
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu			
65	70	75	80
Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp			
85	90	95	
Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu			
100	105	110	
Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn			
115	120	125	
Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val			
130	135	140	
Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln			
145	150	155	160
Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala			
165	170		

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe			
1	5	10	15
Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly			
20	25	30	
Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg			
35	40	45	
Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys			
50	55	60	

Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn
 65 70 75 80
 Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys
 85 90 95
 Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
 100 105 110
 Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser
 115 120 125
 Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
 130 135 140
 Gly Leu Arg Ser Leu Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys
 145 150 155 160
 Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser
 165 170

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg
 1 5 10 15
 Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu
 20 25 30
 Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu
 35 40 45
 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 50 55 60
 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 65 70 75 80
 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 85 90 95
 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 100 105 110
 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 115 120 125
 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 130 135 140
 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 145 150 155 160
 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala
 165 170

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 1 5 10 15
 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
 20 25 30
 Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile
 35 40 45
 Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala
 50 55 60
 Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
 65 70 75 80
 Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met
 85 90 95
 Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu
 100 105 110
 Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln

115		120		125											
Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu
130					135					140					
Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala
145					150					155					160
Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala						
165										170					

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	
1										10				15		
Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	
										20		25		30		
Arg	Thr	Gly	Asp	Arg	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys		
										35		40		45		
Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	
										50		55		60		
Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	
										65		70		75		80
Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	
										85		90		95		
Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Ser		
										100		105		110		
Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	
										115		120		125		
Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	
										130		135		140		
Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Ala	Lys	Glu	Ala	
										145		150		155		160
Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro						
										165		170				

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	
1										10			15			
Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	
										20		25		30		
Thr	Gly	Asp	Arg	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp		
										35		40		45		
Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	
										50		55		60		
Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	
										65		70		75		80
Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	
										85		90		95		
Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Ser	Glu		
										100		105		110		
Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	
										115		120		125		
Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	
										130		135		140		
Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	
										145		150		155		160
Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu							
										165		170				

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn
1									10					15	
Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr
								20					30		
Gly	Asp	Arg	Gly	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser
								35				45			
Arg	Val	Leu	Glu	Arg	Tyr	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	
								50				60			
Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val
								65				75		80	
Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly
								85				95			
Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Ser	Glu	Ala	
								100				110			
Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu
								115				125			
Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu
								130				140			
Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro
								145				155		160	
Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg						
								165				170			

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AATATCACGA	CGGGCTGTGC	TGAACACTGC	AGCTTGAATG	AGAATATCAC	TGTCCCAGAC	60
ACCAAAAGTTA	ATTTCATATGC	CTGGAAGAGG	ATGGAGGTCCG	GGCAGCAGGC	CGTAGAAGTC	120
TGGCAGGGCC	TGGCCCTGCTG	GTCGGAAGGT	GTCCTGCGGG	GCCAGGCCCT	GTTGGTCAAC	180
TCTTCCCCAGC	CGTGGGAGGCC	CCTGCAGCTG	CATGTGGATA	AAGCCGTCAG	TGGCCTTCGC	240
AGCCTCACCA	CTCTGCTTCG	GGCTCTGGGA	GCCCAGAACG	AAGCCATCTC	CCCTCCAGAT	300
GCGGCCTCAG	CTGCTCCACT	CCGAACAATC	ACTGCTGACA	CTTTCCGCAA	ACTCTTCCGA	360
GTCTACTCCA	ATTTCCTCCG	GGAAAGCTG	AAGCTGTACA	CAGGGGAGGC	CTGCAGGAC	420
GGGGACAGAT	GAGGCGCCGG	CTCCCCCACC	CACGCCTCAT	CTGTGACAGC	CGAGTCCTGG	480
AGAGGTACCT	CTTGGAGGCC	AAGGAGGCCG	AG			512

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATCACGACGG	GCTGTGCTGA	ACACTGCA	TTGAATGAGA	ATATCACTGT	CCCAGACACC	60
AAAGTTAATT	TCTATGCCTG	GAAGAGGATG	GAGGTCGGGC	AGCAGGCCGT	AGAAGTCTGG	120
CAGGGCCTGG	CCCTGCTGTC	GGAAAGCTGTC	CTGCGGGGCC	AGGCCCTGTT	GGTCAACTCT	180
TCCCAGCCGT	GGGAGCCCT	GCAGCTGCAT	TGGGATAAAAG	CCGTCAGTGG	CCTTCGCAGC	240
CTCACCACTC	TGCTTCGGGC	TCTGGGAGCC	CAGAAGGAAG	CCATCTCCC	TCCAGATGCG	300
GCCTCAGCTG	CTCCACTCCG	AAACAACTACT	GCTGACACTT	TCCGCAA	CTTCCGAGTC	360
TACTCCAATT	TCTCCGGGGG	AAAGCTGAAG	CTGTACACAG	GGGAGGCC	CAGGACAGGG	420
GACAGATGAG	GCGGCAGCTC	CCCCCACCAC	GCTCATCTG	TGACAGCCGA	GTCCCTGGAGA	480
GGTACCTCTT	GGAGGCCAAG	GAGGCCGAGA	AT			512

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ACGACGGGCT	GTGCTGAACA	CTGCAGCTTG	AATGAGAATA	TCACTGTCCC	AGACACCAAA	60
GTAAATTCT	ATGCCCTGGAA	GAGGATGGAG	GTCGGGCAGG	AGGCCGTAGA	AGCTCTGGCAG	120
GGCCTGGCCC	TGCTGTGCGGA	AGCTGTCTG	CGGGGCCAGG	CCCTGTGGT	CAACTCTTCC	180
CAGCCGTGGG	AGCCCCCTGCA	GCTGCATGTG	GATAAAGCCG	TCAGTGGCCT	TCGCAGCCTC	240
ACCACTCTGC	TTCGGGCTCT	GGGAGCCAG	AAGGAAGCCA	TCTCCCCCTCC	AGATGCGGCC	300
TCAGCTGCTC	CACTCCGAAC	AATCACTGCT	GACACTTTCC	GCAAACCTCTT	CCGAGTCTAC	360
TCCAATTCTC	TCCGGGGAAA	GCTGAAGCT	TACACAGGGG	AGGCCTGAG	GACAGGGGAC	420
AGATGAGGCG	GCGGCTCCCC	CCACCACGCC	TCATCTGTGA	CAGCCGAGTC	CTGGAGAGGT	480
ACCTCTTGGA	GGCCAAGGAG	GCCGAGAATA	TC			512

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACGGGCTGTG	CTGAACACTG	CAGCTTGAAT	GAGAATATCA	CTGTCCCAGA	CACCAAAGTT	60
AATTCTATG	CCTGGAAGAG	GATGGAGGTC	GGGCAGCAGG	CCGTAGAAGT	CTGGCAGGGC	120
CTGGCCCTGC	TGTCGGAAGC	TGTCTGCGG	GGCCAGGCC	TGTTGGTCAA	CTCTTCCAG	180
CCGTGGGAGC	CCCTGCAGCT	GCATGTGGAT	AAAGCCGTCA	GTGGCCTTCG	CAGCCTCAC	240
ACTCTGCTTC	GGGCTCTGGG	AGCCCAGAAC	GAAGCCATCT	CCCCTCCAGA	TGCGGCCTCA	300
GCTGCTCCAC	TCCGAACAAT	CACTGCTGAC	ACTTTCCGCA	AACTCTCCG	AGTCTACTCC	360
AATTTCCTCC	GGGGAAAGCT	GAAGCTGTAC	ACAGGGGAGG	CTTGCAGGAC	AGGGGACAGA	420
TGAGGGGGCG	GCTCCCCCCTCA	CCACGCTCA	TCTGTGACAG	CCGAGTCTG	GAGAGGTACC	480
TCTTGGGAGGC	CAAGGAGGCC	GAGAATATCA	CG			512

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGCTGTGCTG	AACACTGCAG	CTTGAATGAG	AATATCACTG	TCCCAGACAC	CAAAGTTAAT	60
TTCTATGCCT	GGAAGAGGAT	GGAGGTGGG	CAGCAGGCC	TAGAAGTCTG	GCAGGGCCTG	120
GCCCTGCTGT	CGGAAGCTGT	CCTGCCGGGC	CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	180
TGGGAGCCCC	TGCAGCTGCA	TGTGGATAAA	GCCGTCAGTG	GCCTTCGCAG	CCTCACCACT	240
CTGCTTCGCG	CTCTGGGAGC	CCAGAAGGAA	GCCATCTCCC	CTCCAGATGC	GGCCTCAGCT	300
GCTCCACTCC	GAACAATCAC	TGCTGACACT	TCTCGCAAAC	TCTTCCGAGT	CTACTCCAAT	360
TTCCTCCGGG	AAAAGCTGAA	GCTGTACACA	GGGGAGGCC	GCAGGACAGG	GGACAGATGA	420
GGCGGGCGCT	CCCCCCACCA	CGCCTCATCT	GTGACAGCCG	AGTCCTGGAG	AGGTACCTCT	480
TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	CG			512

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TGTGCTGAAC	ACTGCAGCTT	GAATGAGAAT	ATCACTGTCC	CAGACACCAA	AGTTAATTTC	60
TATGCCCTGGA	AGAGGATGGA	GGTCGGGCAG	CAGGCCGTAG	AAAGTCTGGCA	GGGCCTGGCC	120

CTGCTGTCGG	AAGCTGTCCT	GCGGGGCCAG	GCCCTGTTGG	TCAACTCTTC	CCAGCCGTGG	180
GAGCCCTGC	AGCTGCATGT	GGATAAAAGCC	GTCAGTGGCC	TTCGCAGCCT	CACCACTCTG	240
CTTCGGGCTC	TGGGAGGCCA	GAAGGAAGCC	ATCTCCCTC	CAGATGCCGC	CTCAGCTGCT	300
CCACTCCGAA	CAATCACTGC	TGACACTTTC	CGCAAACCTCT	TCCGAGTCTA	CTCCAATTTC	360
CTCCGGGGAA	AGCTGAAGCT	GTACACAGGG	GAGGCCTGCA	GGACAGGGGA	CAGATGAGGC	420
GGCGGCTCCC	CCCACCACGC	CTCATCTGTG	ACAGCCGAGT	CCTGGAGAGG	TACCTCTTGG	480
AGGCCAAGGA	GGCCGAGAAT	ATCACCGACGG	GC			512

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCTAACACT	GCAGCTTGAA	TGAGAATATC	ACTGTCCCAG	ACACCAAAGT	TAATTCTAT	60
GCCTGGAAGA	GGATGGAGGT	CGGGCAGCAG	GCCGTAGAAC	TCTGGCAGGG	CCTGGCCCTG	120
CTGTCGGAAG	CTGTCCCTGCG	GGGCCAGGCC	CTGTTGGTCA	ACTCTTCCA	GCCGTGGGAG	180
CCCCCTGCAGC	TGCATGTGGA	TAAAGCGTC	AGTGGCCTTC	GCAGCCTCAC	CACTCTGCTT	240
CGGGCTCTGG	GAGCCAGGAA	GGAAAGGCCAT	TCCCCTCCAG	ATGCGGCCTC	AGCTGCTCCA	300
CTCCGAACAA	CACTGTGTA	CACTTCCGC	AAACTCTTC	GAGTCTACTC	CAATTTCCTC	360
CGGGGAAAGC	TGAAGCTGTA	CACAGGGAG	GCTGCAGGA	CAGGGGACAG	ATGAGGCGGC	420
GGCTCCCCCC	ACCACGCCTC	ATCTGTGACA	GCCGAGTCCT	GGAGAGGTAC	CTCTTGGAGG	480
CCAAGGAGGC	CGAGAATATC	ACGACGGGCT	GT			512

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GAACACTGCA	GCTTGAATGA	GAATATCACT	GTCCCAGACA	CCAAAGTTAA	TTTCTATGCC	60
TGGAAGAGGA	TGGAGGTCGG	GCAGCAGGCC	GTAGAAGTCT	GGCAGGGCCT	GGCCCTGCTG	120
TCGGAAGCTG	TCCTGCGGGG	CCAGGCCCTG	TTGGTCAACT	CTTCCCAGCC	GTGGGAGGCC	180
CTGCACTGTC	ATGTGGATAA	AGCCGTCACT	GGCCTTCGCA	GCCTCACAC	TCTGCTTCGG	240
GCTCTGGGAG	CCCAGAGGA	AGCCATCTCC	CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	300
CGAACAACTCA	CTGCTGACAC	TTTCCGAAA	CTCTTCCGAG	TCTACTCCAA	TTTCTCCGG	360
GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	TGCAGGACAG	GGGACAGATG	AGGCGGCGGC	420
TCCCCCCCACC	ACGCCTCATC	TGTGACAGCC	GAGTCCTGGA	GAGGTACCTC	TTGGAGGCCA	480
AGGAGGCCGA	GAATATCAGC	ACGGGCTGTG	CT			512

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CACTGCGAGCT	TGAATGAGAA	TATCACTGTC	CCAGACACCA	AAGTTAATT	CTATGCCTGG	60
AAGAGGATGG	AGGTCGGGCA	GCAGGCCGTA	GAAGTCTGGC	AGGGCCTGGC	CCTGCTGTG	120
GAAGCTGTCC	TGGCGGGCCA	GGCCCTGTG	GTCAACTCTT	CCCAGCCGTG	GGACCCCTG	180
CAGCTGATG	TGGATAAAAGC	CGTCAGTGGC	CTTCGCGAGCC	TCACCACTCT	GCTTCGGGCT	240
CTGGGAGGCC	AGAAGGAAGC	CATCTCCCT	CCAGATGCCG	CCTCAGCTGC	TCCACTCCGA	300
ACAATCACTG	CTGACACTTT	CCGAAACACT	TTCCGAGTCT	ACTCCAATT	CCTCCGGGGA	360
AAGCTGAAGC	TGTACACAGG	GGAGGCCTGC	AGGACAGGGG	ACAGATGAGG	CGGCGGCTCC	420
CCCCACCAACG	CCTCATCTGT	GACAGCCGAG	TCCTGGAGAG	GTACCTCTG	GAGGCCAAGG	480
AGGCCGAGAA	TATCACGACG	GGCTGTGCTG	AA			512

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TGCAGCTTGA	ATGAGAATAT	CACTGTCCCC	GACACCAAAG	TTAATTCTCA	TGCCTGGAA	60
AGGATGGAGG	TCGGGCAGCA	GGCCGTAGAA	GTCCTGGCAGG	GCCTGGCCCT	GCTGTCGGAA	120
GCTGTCCTGC	GGGGCCAGGC	CCTGTTGGTC	AACTCTTCCC	AGCCGTGGGA	GCCCCCTGCAG	180
CTGCATGTGG	ATAAAGCCGT	CAGTGCCTT	CGCAGCCTCA	CCACTCTGCT	TCCGGCTCTG	240
GGAGCCCAGA	AGGAAGCCAT	CTCCCCCTCCA	GATGCGGCC	CAGCTGCTCC	ACTCCGAACA	300
ATCACTGCTG	ACACTTTCCG	CAAACCTCTTC	CGAGTCTACT	CCAATTCTCCT	CCGGGGAAAG	360
CTGAAGCTGT	ACACAGGGGA	GGCCTGCAGG	ACAGGGGACA	GATGAGGCAG	CGGCTCCCCC	420
CACCAAGCCT	CATCTGTGAC	AGCCGAGTCC	TGGAGAGGTA	CCTCTTGAG	GCCAAGGAGG	480
CCGAGAATAT	CACGACGGGC	TGTGCTGAAC	AC			512

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AGCTTGAATG	AGAATATCAC	TGTCCCAGAC	ACCAAAGTTA	ATTTCTATGC	CTGGAAGAGG	60
ATGGAGGTG	GGCAGCAGGC	CGTAGAACGTC	TGGCAGGGCC	TGGCCCTGCT	GTCGGAAGCT	120
GTCCTGCGG	GCCAGGCCCT	GTTGGTCAAC	TCTTCCCAGC	CGTGGGAGCC	CCTGCAGCTG	180
CATGTGGATA	AAGCCGTCA	TGGCCTTCAG	AGCCTCACC	CTCTGCTTCG	GGCTCTGGGA	240
GCCCAAGA	AAGCCATCTC	CCCTCCAGAT	GGCCGCTCAG	CTGCTCCACT	CCGAACAATC	300
ACTGCTGACA	CTTTCCGCAA	ACTCTTCCG	GTCTACTCCA	ATTTCTCCG	GGGAAAGCTG	360
AAGCTGTACA	CAGGGGAGGC	CTGCAGGACA	GGGGACAGAT	GAGGCAGCAG	CTCCCCCCCAC	420
CACGCCCTCAT	CTGTGACAGC	CGAGTCTCTG	AGAGGTACCT	CTTGGAGGCC	AAGGAGGCCG	480
AGAATATCAC	GACGGGCTGT	GCTGAACACT	GC			512

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TTGAATGAGA	ATATCACTGT	CCCAGACACC	AAAGTTAATT	TCTATGCCTG	GAAGAGGATG	60
GAGGTCGGGC	AGCAGGCCGT	AGAAGTCTGG	CAGGGCCTGG	CCCTGCTGTC	GGAAGCTGTG	120
CTGCGGGGCC	AGCCTCTGTT	GGTCAACTCT	TCCCAGCGGT	GGGAGCCCT	GCAGCTGCAT	180
GTGGATAAAAG	CCGTCAAGTGG	CCTTCGCAGC	CTCACCACTC	TGCTTGGGGC	TCTGGGAGCC	240
CAGAAGGAAG	CCATCTCCCC	TCCAGATGCG	GCCTCAGCTG	CTCCACTCCG	AAACAATCACT	300
GCTGACACTT	TCCGCAAAC	CTTCCGAGTC	TACTCCAATT	TCCTCCGGG	AAAGCTGAAG	360
CTGTACACAG	GGGAGGCCCTG	CAGGACAGGG	GACAGATGAG	GCGGCGGCTC	CCCCCACAC	420
GCCTCATCTG	TGACAGCCGA	GTCCTGGAGA	GGTACCTCTT	GGAGGCCAAG	GAGGCCGAGA	480
ATATCACGAC	GGGCTGTGCT	GAACACTGCA	GC			512

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AATGAGAATA	TCACTGTCCC	AGACACCAAA	GTAAATTCT	ATGCCTGGAA	GAGGATGGAG	60
GTCGGGCAGC	AGGCCGTAGA	AGTCTGGCAG	GGCCTGGCCC	TGCTGTCGGA	AGCTGTCCTG	120
CGGGGCCAGG	CCCTGTTGGT	CAACTCTTCC	CAGCCGTGGG	AGCCCCCTGCA	GCTGCATGTG	180
GATAAAGCCG	TCAGTGGCCT	TCGCAGCCTC	ACCACTCTGC	TTCGGGCTCT	GGGAGCCCGAG	240
AAGGAAGCCA	TCTCCCTCC	AGATGCGGCC	TCAGCTGCTC	CACTCCGAAC	AATCACTGCT	300
GACACTTTCC	GCAAACCTCTT	CCGAGTCTAC	TCCAATTCTC	TCCGGGAAA	GCTGAAGCTG	360
TACACAGGGG	AGGGCTGCA	AGCAGGGGAC	AGATGAGGCG	GCGGCTCCCC	CCACCAAGGCC	420
TCATCTGTGA	CAGCCGAGTC	CTGGAGGGT	ACCTCTTGG	GGCCAAGGAG	GCCGAGAATA	480
TCACCGACGGG	CTGTGCTGAA	CACTGCAGCT	TG			512

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAGAATATCA	CTGTCCCAGA	CACCAAAGTT	AATTCTATG	CCTGGAAGAG	GATGGAGGTC	60
GGGCAGCAGG	CCGTAGAAAGT	CTGGCAGGGC	CTGGCCCTGC	TGTCGGAAGC	TGTCCCTGCGG	120
GGCCAGGCC	TGTTGGCTAA	CTCTTCCCAG	CCGTGGGAGC	CCCTGCAGCT	GCATGTGGAT	180
AAAGCCGTCA	GTGGCCTTCG	CAGCCTCAC	ACTCTGCTTC	GGGCTCTGGG	AGCCCCAGAAG	240
GAAGCCATCT	CCCCTCCAGA	TGCGGCCCTA	GCTGCTCCAC	TCCGAACAAT	CACTGCTGAC	300
ACTTTCCGCA	AACTCTTCCG	AGTCTACTCC	AATTCTCTCC	GGGGAAAGCT	GAAGCTGTAC	360
ACAGGGGAGG	CCTGCAGGAC	AGGGGACAGA	TGAGGCAGGC	GCTCCCCCA	CCACGCCCTCA	420
TCTGTGACAG	CCGAGTCCTG	GAGAGGTACC	TCTTGGAGGC	CAAGGAGGCC	GAGAATATCA	480
CGACGGGCTG	TGCTGAACAC	TGCAGCTTGA	AT			512

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AATATCACTG	TCCCAGACAC	CAAAGTTAAT	TTCTATGCCT	GGAAGAGGGAT	GGAGGTCGGG	60
CAGCAGGCC	TAGAAGTCTG	GCAGGGCCTG	GCCCTGCTGT	CGGAAGCTGT	CCTGCGGGGC	120
CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	TGGGAGCCCC	TGCAGCTGCA	TGTGGATAAA	180
GCCGTCACTG	GCCTTCGCG	CCTCACCACT	CTGCTTCGGG	CTCTGGGAGC	CCACAAGGAA	240
GCCATCTCCC	CTCCAGATGC	GGCCTCAGCT	GCTCCACTCC	GAACAATCAC	TGCTGACACT	300
TTCCGAAAC	TCTTCCGAGT	CTACTCCAAT	TTCCCTCCGGG	GAAAGCTGAA	GCTGTACACA	360
GGGGAGGCC	GCAGGACAGG	GGACAGATGA	GGCGGGCGCT	CCCCCACCA	CGCCTCATCT	420
GTGACAGCCG	AGTCTTGGAG	AGGTACCTCT	TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	480
CGGGCTGTGC	TGAACACTGC	ACCTTGAATG	AG			512

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ATCACTGTCC	CAGACACCAA	AGTTAATTTC	TATGCCCTGGA	AGAGGATGGA	GGTCGGGCAG	60
CAGGCCGTAG	AAGTCTGGCA	GGGCCTGGCC	CTGCTGTCGG	AAGCTGTCT	GCGGGGCCAG	120
GCCCTGTTGG	TCAACTCTTC	CCAGCCGTGG	GAGCCCCCTGC	AGCTGCATGT	GGATAAAGCC	180
GTCAGTGGCC	TTCGCAGCCT	CACCACTCTG	CTTCGGGCTC	TGGGAGCCCA	GAAGGAAGCC	240
ATCTCCCTC	CAGATGCGGC	CTCAGCTGCT	CCACTCCGAA	CAATCACTGC	TGACACTTTG	300
CGCAAACCTCT	TCCGAGTCTA	CTCCAATTTC	CTCCGGGGAA	AGCTGAAGCT	GTACACAGGG	360
GAGGCCCTGCA	GGACAGGGGA	CAGATGAGGC	GGCGGCTCCC	CCCACCAAGC	CTCATCTGTG	420
ACAGCCGAGT	CCTGGAGAGG	TACCTTGTGG	AGGCCAAGGA	GGCGGAGAAT	ATCACGACGG	480
GCTGTGCTGA	ACACTGCAGC	TTGAATGAGA	AT			512

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ACTGTCCCAG	ACACCAAAGT	TAATTCTAT	GCCTGGAAGA	GGATGGAGGT	CGGGCAGCAG	60
GGCGTAGAAC	TCTGGCAGGG	CCTGGCCCTG	CTGTCGGAAG	CTGTCCCTGCG	GGGCCAGGCC	120

CTGTTGGTCA	ACTCTTCCCCA	GCCGTGGGAG	CCCCTGCAGC	TGCATGTGGA	TAAAGCCGTC	180
AGTGGCCTTC	GCAGCCTCAC	CACTCTGCTT	CGGGCTCTGG	GAGCCCAGAA	GGAAGCCATC	240
TCCCCCTCCAG	ATGCGGCCCTC	AGCTGCTCCA	CTCCGAACAA	TCACTGCTGA	CACTTTCCGC	300
AAACTCTTCC	GAGTCTACTC	CAATTTCCTC	CGGGGAAAGC	TGAAGCTGTA	CACAGGGGAG	360
GCCTGCAGGA	CAGGGGACAG	ATGAGGGCGGC	GGCTCCCCCC	ACCACGCCCTC	ATCTGTGACA	420
GCCGAGT CCT	GGAGAGGTAC	CTCTTGAGG	CCAAGGAGGC	CGAGAATATC	ACGACGGGCT	480
GTGCTGAACA	CTGCAGCTTG	AATGAGAATA	ATC			513

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GTCCCAGACA	CCAAAGTTAA	TTTCTATGCC	TGGAAGAGGA	TGGAGGTGCG	GCAGCAGGCC	60
GTAGAACGCT	GGCAGGGCCT	GGCCCTGCTG	TCGGAAGCTG	TCCTGCGGGG	CCAGGCCCTG	120
TTGGTCAACT	CTTCCCAGCC	GTGGGAGCCC	CTGCAGCTGC	ATGTGGATAA	AGCCGTCAGT	180
GGCCTTCGCA	GCCTCACAC	TCTGCTTCGG	GCTCTGGGAG	CCCAGAAGGA	AGCCATCTCC	240
CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	CGAACAAATCA	CTGCTGACAC	TTTCCGCAAA	300
CTCTTCCGAG	TCTACTCCAA	TTTCCTCCGG	GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	360
TGCAGGACAG	GGGACAGATG	AGGCGCGGC	TCCCCCCCAC	ACGCCTCATC	TGTGACAGCC	420
GAGTCTGGA	GAGGTACCTC	TTGGAGGCCA	AGGAGGCCGA	GAATATCACG	ACGGGCTGTG	480
CTGAACACTG	CAGCTTGAAT	GAGAATAATC	ACT			513

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCAGACACCA	AAGTTAATT	CTATGCCCTGG	AAGAGGATGG	AGGTCGGGCA	GCAGGCCGTA	60
GAAGTCTGGC	AGGGCCTGGC	CCTGCTGTG	GAAGCTGTCC	TGCGGGGCCA	GGCCCTGTTG	120
GTCAACTCTT	CCCAGCCGTG	GGAGCCCCTG	CAGCTGCATG	TGGATAAAGC	CGTCAGTGGC	180
CTTCGAGGCC	TCACTACTCT	GCTTCGGGCT	CTGGGAGGCC	AGAAGGAAGC	CATCTCCCT	240
CCAGATGCGG	CCTCAGCTGC	TCCACTCCGA	ACAATCACTG	CTGACACTTT	CCGCAAACTC	300
TTCCGAGTCT	ACTCCAATT	CCTCCGGGGA	AAAGCTGAAGC	TGTACACAGG	GGAGGCCCTGC	360
AGGACAGGGG	ACAGATGAGG	CGGCGCCTCC	CCCCACCAAG	CCTCATCTGT	GACAGCCGAG	420
TCCTGGAGAG	GTACCTCTTG	GAGGCCAAGG	AGGCCGAGAA	TATCACGACG	GGCTGTGCTG	480
AACACTGCAG	CTTGAATGAG	AATAATCACT	GTC			513

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GACACCAAAG	TTAATTCTA	TGCCTGGAAG	AGGATGGAGG	TCGGGCAGCA	GGCCGTAGAA	60
GTCTGGCAGG	GCCTGGCCCT	GCTGTCGGAA	GCTGTCCTGC	GGGGCCAGGC	CCTGTTGGTC	120
AACTCTTCCC	AGCCGTGGGA	GCCCCTCGAG	CTGCATGTGG	ATAAAGCCGT	CAGTGGCCTT	180
CGCAGCCTCA	CAACTCTGCT	TCGGGCTCTG	GGAGCCCAGA	AGGAAGCCAT	CTCCCCCTCCA	240
GATGCGGCC	CAGCTGCTC	ACTCCGAACA	ATCACTGCTG	ACACTTCCG	CAAACACTCTTC	300
CGAGTCTACT	CCAATTCCCT	CCGGGAAAG	CTGAAGCTGT	ACACAGGGGA	GGCCTGCAGG	360
ACAGGGGACA	GATGAGGCAGG	CGGCTCCCCC	CACCACGCCT	CATCTGTGAC	AGCCGAGTCC	420
TGGAGAGGTA	CCTCTTGGAG	GCCAAGGAGG	CCGAGAATAT	CACGACGGGC	TGTGCTGAAC	480
ACTGCAGCTT	GAATGAGAAT	AATCACTGTC	CCA			513

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AGGATGGAGG	TGGGGCAGCA	GGCGTAGAA	GTCCTGGCAGG	GCCTGGCCCT	GCTGTGGAA	60
GCTGTCTGC	GGGGCCAGGC	CCTGTTGGTC	AACTCTTCCC	AGCCGTGGGA	GCCCTGCGAG	120
CTGCATGTGG	ATAAAGCCGT	CAGTGGCCTT	CGCAGCCTCA	CCACTCTGCT	TCGGGCTCTG	180
GGAGCCCCAGA	AGGAAGCCAT	CTCCCCCTCCA	GATGCGGCCCT	CAGCTGCTCC	ACTCCGAACA	240
ATCACTGCTG	ACACTTTCCG	CAAACCTCTC	CGAGTCTACT	CCAATTTCCT	CCGGGGAAAG	300
CTGAAGCTGT	ACACAGGGGA	GCCCTGCGAGG	ACAGGGGACA	GATGAGGCAGG	CGGCTCCCCC	360
CACCAAGCCT	CATCTGTGAC	AGCCGAGTCC	TGGAGAGGTA	CCTCTGGAG	GCCAAGGAGG	420
CCGAGAATAT	CACGACGGGC	TGTGCTGAAC	ACTGCAGCTT	GAATGAGAAT	AATCACTGTC	480
CCAGACACCA	AAGTAAATT	CTATGCCTGG	AAG			513

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ATGGAGGTCG	GGCAGCAGGGC	CGTAGAACGTC	TGGCAGGGCC	TGGCCCTGCT	GTCGGAAGCT	60
GTCCTGCGGG	GCCAGGCCCT	GTTGGTCAAC	TCTTCCCAGC	CGTGGGAGCC	CCTGCAGCTG	120
CATGTGGATA	AAGCCGTCAG	TGGCCTTCGCG	AGCCTCACCA	CTCTGCTTCG	GGCTCTGGGA	180
GCCCAGAAGG	AAGCCATCTC	CCCTCAGAT	GGGGCCTCAG	CTGCTCCACT	CCGAACAATC	240
ACTGCTGACA	CTTTCGCATA	ACACTTCCG	GTCCTACTCCA	ATTTCCTCCG	GGGAAAGCTG	300
AAGCTGTACA	CAGGGGAGGC	CTGCAGGACA	GGGGACAGAT	GAGGCGGCAG	CTCCCCCAC	360
CACGCCTCAT	CTGTGACAGC	CGAGTCTGG	AGAGGTACCT	CTTGGAGGCC	AAGGAGGCCG	420
AGAATATCAC	GACGGGCTGT	GCTGAACACT	GCAGCTTGAA	TGAGAATAAT	CACTGTCCCA	480
GACACCAAAG	TTAATTCTCA	TGCGCTGGAA	AGG			513

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAGGTCGGGC	AGCAGGCCGT	AGAAGTCTGG	CAGGGCCTGG	CCCTGCTGTC	GGAAGCTGTC	60
CTGGGGGGCC	AGGCCCTGTT	GGTCAACTCT	TCCCAGCCGT	GGGAGCCCT	GCAGCTGCAT	120
GTGGGATAAAAG	CCGTCACTG	CCTTCGAGC	CTCACCACTC	TGCTTCGGGC	TCTGGGAGCC	180
CAGAAGGAAG	CCATCTCCCC	TCCAGATGCG	GCTCAGCTG	CTCCACTCCG	AACAATCACT	240
GCTGACACTT	TCCGCAAAC	CTTCCGAGTC	TACTCCAATT	TCCTCCGGGG	AAAGCTGAAG	300
CTGTACACAG	GGGAGGCCTG	CAGGACAGGG	GACAGATGAG	GCAGCGGCTC	CCCCCACCAC	360
GCCTCATCTG	TGACAGGCCA	GTCCTGGAGA	GGTACCTCTT	GGAGGCCAAG	GAGGCGAGA	420
ATATCACGAC	GGGCTGTGCT	GAACACTGCA	GCTTGAATGA	GAATAATCAC	TGTCCCGAC	480
ACCAAAGTTA	ATTTCATGCA	CTGGAAGAGG	ATG			513

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GTCGGGCAGC	AGGCCGTAGA	AGTCTGGCAG	GGCCTGGCCC	TGCTGTGGAA	AGCTGTCTG	60
CGGGGCCAGG	CCCTGTTGGT	CAACTCTTCC	CAGCCGTGGG	AGCCCTGCA	GCTGCATGTG	120
GATAAAGCCG	TCAGTGGCT	TCGCAGCCTC	ACCACTCTG	TTCGGGCTCT	GGGAGCCAG	180
AAGGAAGCCA	TCTCCCTC	AGATGCGGCC	TCAGCTGCTC	CACTCCGAAC	AATCACTGCT	240
GACACTTTCC	GAAACTCTT	CCGAGTCTAC	TCCAATTTC	TCCGGGGAAA	GCTGAAGCTG	300
TACACAGGGG	AGGCCTGAG	GACAGGGGAC	AGATGAGGCG	GCAGCGCC	CCACCAAGGCC	360
TCATCTGTGA	CAGCCGAGTC	CTGGAGAGGT	ACTCTTGG	GGCCAAGGAG	GCCGAGAATA	420
TCACGACGGG	CTGTGCTGAA	CACTGAGCT	TGAATGAGAA	TAATCACTGT	CCCAGACACC	480
AAAGTTAATT	TCTATGCCTG	GAAGAGGATG	GAG			513

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	TGGGAGCCCC	TGCAGCTGCA	TGTGGATAAA	60
GCCGTCAGTG	GGCTTCGCG	CCTCACCACT	CTGCTTCGGG	CTCTGGGAGC	CCAGAACGAA	120
GCCATCTCCC	CTCCAGATGC	GGCTCAGACT	GCTCCACTCC	GAACAATCAC	TGCTGACACT	180
TTCCGCAAAC	TCTTCCGAGT	CTACTCCAAT	TTCCCTCCGGG	GAAAGCTGAA	GCTGTACACA	240
GGGGAGGCC	GCAGGACAGG	GGACAGATGA	GGCGGCGGCT	CCCCCCCACCA	CGCCTCATCT	300
GTGACAGCCG	AGTCCTGGAG	AGGTACCTCT	TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	360
CGGGCTGTGC	TGAACACTGC	AGCTTGAATG	AGAATAATCA	CTGTCCCAGA	CACCAAAGTT	420
AATTCTATG	CCTGGAAGAG	GATGGAGGTC	GGGCAGCAGG	CCGTAGAAAGT	CTGGCAGGGC	480
CTGGCCCTGC	TGTCGGAAGC	TGTCCCTGCGG	GGC			513

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GCCCTGTTGG	TCAACTCTTC	CCAGCCGTGG	GAGCCCCCTGC	AGCTGCATGT	GGATAAAAGCC	60
GTCAGTGGCC	TTCGCAGCCT	CAACCACTCTG	CTTCGGGCTC	TGGGAGCCA	GAAGGAAGCC	120
ATCTCCCCTC	CAGATGCGGC	CTCAGCTGCT	CCACTCCGAA	CAATCACTGC	TGACACTTTTC	180
CGCAAACCTCT	TCCGAGTCTA	CTCCAATTTC	CTCCGGGGAA	AGCTGAAGCT	GTACACAGGG	240
GAGGCCTGCA	GGACAGGGGA	CAGATGAGGC	GGCGGCTCCC	CCCACCACGC	CTCATCTGTG	300
ACAGCCGAGT	CCTGGAGAGG	TACCTCTTG	AGGCCAAGGA	GGCCGAGAAT	ATCACGACGG	360
GCTGTGCTGA	ACACTGCAGC	TTGAATGAGA	ATAATCACTG	TCCCAGACAC	CAAAGTTAAT	420
TTCTATGCC	GGAAGAGGAT	GGAGGTGGG	CAGCAGGCCG	TAGAAGTCTG	GCAGGGCCTG	480
GCCCTGCTGT	CGGAAGCTGT	CCTGCCGGGC	CAG			513

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTGTTGGTCA	ACTCTTCCCA	GCCGTGGGAG	CCCCTGCAGC	TGCATGTGGA	TAAAGCCGTC	60
AGTGGCCTTC	GCAGCCTCAC	CACTCTGCTT	CGGGCTCTGG	GAGCCAGAA	GGAAAGCCATC	120
TCCCCCTCCAG	ATGCGGCCTC	AGCTGCTCCA	CTCCGAACAA	TCACTGCTGA	CACTTTCCGC	180
AAAACCTTCC	GAGTCTACTC	CAATTTCCTC	CGGGGAAAGC	TGAAGCTGTA	CACAGGGGAG	240
GCCTGCGAGG	CAGGGGACAG	ATGAGGGCGC	GGCTCCCCCCC	ACCACGCCCTC	ATCTGTGACA	300
GCCGAGTCCT	GGAGAGGTAC	CTCTTGAGG	CCAAGGAGGC	CGAGAATATC	ACGACGGGCT	360
GTGCTGAACA	CTGCAAGCTTG	AATGAGAATA	ATCACTGTC	CAGACACCAA	AGTTAATTTC	420
TATGCCTGGA	AGAGGATGGA	GGTCGGGCAG	CAGGCCGTAG	AACTCTGGCA	GGGCCTGGCC	480
CTGCTGTCGG	AAGCTGTCCT	GGGGGCCAG	GCC			513

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TTGGTCAACT	CTTCCCAGCC	GTGGGAGCCC	CTGCAGCTGC	ATGTGGATAA	AGCCGTCAGT	60
GGCCTCGCA	GCCTCACCA	TCTGCTTCGG	GCTCTGGGAG	CCCAGAACGA	AGCCATCTCC	120

CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	CGAACAAATCA	CTGCTGACAC	TTTCCGCAA	180
CTCTTCCGAG	TCTACTCCAA	TTTCCTCCGG	GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	240
TGCAGGACAG	GGGACAGATG	AGGCAGCGGC	TCCCCCCCACC	ACGCCTCATC	TGTGACAGCC	300
GAGTCCTGGA	GAGGTACCTC	TTGGAGGCCA	AGGAGGCCGA	GAATATCACG	ACGGGCTGTG	360
CTGAACACTG	CAGCTTGAAT	GAGAATAATC	ACTGTCCCAG	ACACCAAAGT	TAATTCTAT	420
GCCTGGAAGA	GGATGGAGGT	CGGGCAGCAG	GCCCTAGAAG	TCTGGCAGGG	CCTGGCCCTG	480
CTGTCGGAAG	CTGTCCTGCG	GGGCCAGGCC	CTG			513

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTCAACTCTT	CCCAGCCGTG	GGAGCCCCTG	CAGCTGCATG	TGGATAAAAGC	CGTCAGTGGC	60
CTTCGAGCC	TCACCACTCT	GCTTCGGGCT	CTGGGAGGCC	AGAAGGAAGC	CATCTCCCT	120
CCAGATGCCG	CCTCAGCTGC	TCCACTCCGA	ACAATCACTG	CTGACACTTT	CCGAAACACTC	180
TTCCGAGTCT	ACTCCAATT	CCTCCGGGGA	AAGCTGAAGC	TGTACACAGG	GGAGGCCTGC	240
AGGACAGGGG	ACAGATGAGG	CGGCGCTCAG	CCCCACCACG	CCTCATCTGT	GACAGCCGAG	300
TCCTGGAGAG	GTACCTCTTG	GAGGCCAAGG	AGGCGAGAGAA	TATCACGACG	GGCTGTGCTG	360
AACACTGCAG	CTTGAATGAG	AATAATCACT	GTCCCCAGACA	CCAAAGTTAA	TTTCTATGCC	420
TGGAAGAGGA	TGGAGGTGG	GCACCGAGCC	GTAGAAGTCT	GGCAGGGCCT	GGCCCTGCTG	480
TCGGAAGCTG	TCCTGCGGGG	CCAGGCCCTG	TTG			513

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AACTCTTCCC	AGCCGTGGGA	GCCCCTGCAG	CTGCATGTGG	ATAAAGCCGT	CAGTGGCCTT	60
CGCAGCCTCA	CCACTCTGCT	TCGGGCTCTG	GGAGCCCCAGA	AGGAAGCCAT	CTCCCCCTCCA	120
GATGCGGCCT	CAGCTGCTCC	ACTCCGAACA	ATCACTGCTG	ACACTTCCG	CAAACCTTTC	180
CGAGTCTACT	CCAATTTCCT	CCGGGAAAG	CTGAAGCTGT	ACACAGGGGA	GGCTGTGAGG	240
ACAGGGGACA	GATGAGGGCGG	CGCGCTCCCC	CACCAAGCCT	CATCTGTGAC	AGCCGAGTCC	300
TGGAGGAGTA	CCTCTTGGAG	GCCAAAGGAGG	CCGAGAATAT	CACGACGGGC	TGTGCTGAAC	360
ACTGCAGCTT	GAATGAGAAT	AATCACTGTC	CCAGACACCA	AAGTTAATT	CTATGCCCTGG	420
AAGAGGATGG	AGGTCTGGCA	GCAGGCCGTA	GAAGTCTGGC	AGGGCCTGGC	CCTGCTGTGCG	480
GAAGCTGTCC	TGCGGGGCCA	GGCCCTGTTG	GTC			513

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TCTTCCCAGC	CGTGGGAGCC	CCTGCAGCTG	CATGTGGATA	AAGCCGTAG	TGGCCTTCGC	60
AGCCTCACCA	CTCTGCTTCG	GGCTCTGGGA	GCCCAGAAGG	AAGCCATCTC	CCCTCCAGAT	120
GCGGCTCTAG	CTGCTCCACT	CCGAACAATC	ACTGCTGACA	CTTTCCGCAA	ACTCTTCCGA	180
GTCTACTCCA	ATTTCCCTCG	GGGAAAGCTG	AAGCTGTACA	CAGGGGAGGC	CTGCAGGACA	240
GGGGACAGAT	GAGGCAGCGG	CTCCCCCCCAC	CACGCCTCAT	CTGTGACAGC	CGAGTCCTGG	300
AGAGGTACCT	CTTGGAGGCC	AAGGAGGCCG	AGAATATCAC	GACGGGCTGT	GCTGAACACT	360
GCAGCTTGAA	TGAGAATAAT	CACTGTCCCA	GACACCAAAG	TTAATTCTA	TGCCTGGAAG	420
AGGATGGAGG	TCGGGCAGCA	GGCCGTAGAA	GTCTGGCAGG	GCCTGGCCCT	GCTGTCGGAA	480
GCTGTCCTGC	GGGCCAGGC	CCTGTTGGTC	AAC			513

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCCCAGCCGT	GGGAGCCCC	GCAGCTGCAT	GTGGATAAAG	CCGTCA	GTCAGTGG	CCTTCGCAGC	60
CTCACCACTC	TGCTTCGGGC	TCTGGGAGCC	CAGAAGGAAG	CCATCTCCC	TCCAGATGCG	120	
GCCTCAGCTG	CTCCACTCCG	AACAATCACT	GCTGACACTT	TCCGAAACT	CTTCCGAGTC	180	
TACTCCAATT	TCTCTCGGGG	AAAGCTGAAG	CTGTACACAG	GGGAGGCC	CAGGACAGGG	240	
GACAGATGAG	GCGGCGGCTC	CCCCCACAC	GCCTCATCTG	TGACAGCGA	GTCCTGGAGA	300	
GGTACCTCTT	GGAGGCCAAG	GAGGCCGAGA	ATATCACGAC	GGGCTGTGCT	GAACACTGCA	360	
GCTTGAAATGA	GAATAATCAC	TGTCCCAGAC	ACCAAAGTTA	ATTTCATGC	CTGGAAGAGG	420	
ATGGAGGTCG	GCGAGCAGGC	CGTAGAACGTC	TGGCAGGGCC	TGGCCCTGCT	GTCGGAAGCT	480	
GTCCTCGGGG	GCCAGGCC	GTTGGTCAAC	TCT			513	

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CAGCCGTGGG	AGCCCCCTGCA	GCTGCATGTG	GATAAAGCCG	TCAGTGGCCT	TCGCAGCCTC	60
ACCACCTCTGC	TTCGGGCTCT	GGGAGCCCAG	AAGGAAGCCA	TCTCCCTCC	AGATGCGGCC	120
TCAGCTGCTC	CACTCCGAA	AATCACTGCT	GACACTTTCC	GCAAACCTTT	CCGAGTCTAC	180
TCCAATTCTC	TCCGGGGAAA	GCTGAAGCTG	TACACAGGGG	AGGCCTGAG	GACAGGGGAC	240
AGATGAGGCG	GCGGCTCCCC	CCACCAAGCC	TCATCTGTGA	CAGCCGAGTC	CTGGAGAGGT	300
ACCTCTTCCA	GGCCAAGGAG	GCCGAGAATA	TCACGACGGG	CTGTGCTGAA	CACTGCAGCT	360
TGAATGAGAA	TAATCACTGT	CCCAGACACC	AAAGTTAATT	TCTATGCC	GAAGAGGATG	420
GAGGTCGGGC	AGCAGGCCGT	AGAAGTCTGG	CAGGGCCTGG	CCCTGCTGTC	GGAAGCTGTC	480
CTGCGGGGCC	AGGCCCTGTT	GGTCAACTCT	TCC			513

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CCGTGGGAGC	CCCTGCAGCT	GCATGTGGAT	AAAGCCGTCA	GTGGCCTTCG	CAGCCTCACC	60
ACTCTGCTTC	GGGCTCTGGG	AGGCCAGAG	GAAGCCATCT	CCCCTCCAGA	TGGGCCCTCA	120
GCTGCTCCAC	TCCGAACA	CACTGCTGAC	ACTTCCGCA	AACTCTCCG	AGTCTACTCC	180
AATTCTCTCC	GGGGAAAGCT	GAAGCTGTAC	ACAGGGGAGG	CCTGCAGGAC	AGGGGACAGA	240
TGAGGCGGGC	GCTCCCCCA	CCACGCC	TCTGTGACAG	CCGAGTCTG	GAGAGGTACC	300
TCTTGGAGGC	CAAGGAGGCC	GAGAATATCA	CGACGGGCTG	TGCTGAAACAC	TGCAGCTTG	360
ATGAGAATAA	TCACTGTCCC	AGACACCAAA	GTTAATTCT	ATGCCTGGAA	GAGGATGGAG	420
GTCGGGCAGC	AGGCCGTAGA	AGTCTGGCAG	GGCCTGGCCC	TGCTGTCGGA	AGCTGCTCTG	480
CGGGGCCAGG	CCCTGTTGGT	CAACTCTTCC	CAG			513

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TGGGAGCCC	TGCAGCTGCA	TGTGGATAAA	GCCGTCAGTG	GCCTTCGCAG	CCTCACCAC	60
CTGCTTCGGG	CTCTGGGAGC	CCAGAAGGA	GCCATCTCCC	CTCCAGATGC	GGCCTCAGCT	120
GCTCCACTCC	GAACAATCAC	TGCTGACACT	TTCCGCAAAC	TCTTCCGAGT	CTACTCCAAT	180
TTCCCTCGGG	AAAAGCTGAA	GCTGTACACA	GGGGAGGCC	GCAGGACAGG	GGACAGATGA	240
GGCGCGGGCT	CCCCCCACCA	CGCCTCATCT	GTGACAGCCG	AGTCCTGGAG	AGGTACCTCT	300
TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	CGGGCTGTGC	TGAACACTGC	AGCTTGAATG	360
AGAATAATCA	CTGTCCCAGA	ACACAAAGTT	AATTCTATG	CCTGGAAAGAG	GATGGAGGTC	420
GGGCAGCAGG	CCGTAGAACGTC	CTGGCAGGGC	CTGGCCCTG	TGTCGGAAGC	TGTCCCTGCGG	480
GGCCAGGCC	TGTTGGTCAA	CTCTTCCCAG	CCG			513

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GAGCCCTGC	AGCTGCATGT	GGATAAAGCC	GTCA	GTGGCC	TTCGCAGCCT	CACCA	ACTCTG	60
CTTCGGGCTC	TGGGAGGCCA	GAAGGAAGCC	ATCTCCC	CTC	CAGATGCGC	CTC	AGCTG	120
CCACTCGAA	CAATCACTGC	TGACACTTTC	CGCAA	ACTCT	TCCGAGTCTA	CTCC	AAATTTC	180
CTCCGGGAA	AGCTGAAGCT	GTACACAGGG	GAGG	CCTGCA	GGACAGGG	CAGATGAGG	C	240
GGCGGCTCCC	CCCACCACGC	CTCATCTGTG	ACAGCCGAGT	CCTGGAGAGG	TAC	CTCTTGG	300	
AGGCCAAGGA	GGCCGAGAA	ATCACGACGG	GCTGTGCTGA	ACACTGCAGC	TTGAATGAGA	360		
ATAATCACTG	TCCCAGACAC	CAAAGTTAAT	TTCTATGCCT	GGAAGAGGAT	GGAGGTG	GGG	420	
CAGCAGGCCG	TAGAAGTCTG	GCAGGGCCTG	GCCCTGCTGT	CGGAAGCTGT	CCTGC	GGGGC	480	
CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	TGG					513

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTTCGGGCTC	TGGGAGGCCA	GAAGGAAGCC	ATCTCCC	CTC	CAGATGCGC	CTC	AGCTG	60
CCACTCCGAA	CAATCACTGC	TGACACTTTC	CGCAA	ACTCT	TCCGAGTCTA	CTCC	AAATTTC	120
CTCCGGGAA	AGCTGAAGCT	GTACACAGGG	GAGG	CCTGCA	GGACAGGG	CAGATGAGG	C	180
GGCGGCTCCC	CCCACCACGC	CTCATCTGTG	ACAGCCGAGT	CCTGGAGAGG	TAC	CTCTTGG	240	
AGGCCAAGGA	GGCCGAGAA	ATCACGACGG	GCTGTGCTGA	ACACTGCAGC	TTGAATGAGA	300		
ATAATCACTG	TCCCAGACAC	CAAAGTTAAT	TTCTATGCCT	GGAAGAGGAT	GGAGGTG	GGG	360	
CAGCAGGCCG	TAGAAGTCTG	GCAGGGCCTG	GCCCTGCTGT	CGGAAGCTGT	CCTGC	GGGGC	420	
CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	TGGGAGCCC	TGCAGCTGCA	TGTGGATAAA	480		
GCGTCAGTG	GCCTTCGCA	CCTCACCACT	CTG					513

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGGGCTCTGG	GAGCCCAGAAA	GGAA	GGCCATC	TCCC	CTCCAG	ATGCG	GCCTC	AGCTG	CTCCA	60
CTCCGAACAA	TCACTGCTGA	CACTT	CCGC	AAACT	CTTCC	GAGT	CTACTC	CAAT	TTCC	120
CGGGGAAAGC	TGAAGCTGTA	CACAGGGAG	GCCT	GCAGGA	CAGGG	GACAG	ATGAGG	CGGC	180	
GGCTCCCCCC	ACCACGCCTC	ATCTGTGACA	GCCG	AGTCCT	GGAG	AGGTAC	CTCT	TGGAGG	240	
CCAAGGAGCC	CGAGAAATTC	ACGACGGGCT	GTG	CTGAACA	CTG	CAGCTTG	AATGAGA	ATA	300	
ATCACTGTC	ACGACACCAA	AGTTAATTTC	TATG	CCCTGGA	AGAGG	ATGGA	GGT	CGGGCAG	360	
CAGGCCGTAG	AAGTCTGGCA	GGG	CCTGGC	CTG	CTGTC	GG	AAGCT	GCCT	420	
GCCCTGTTGG	TCAACTCTTC	CCAGCCGTGG	GAG	CCCCTGC	AG	CTGCA	TG	GGATAAAGCC	480	
GTCAGTGGCC	TCAGCAGCCT	CACCA	CTG						513	

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCTCTGGGAG	CCCAGAAGGAA	AGCC	CATCTCC	CCTCC	AGATG	CGGC	CTCAGC	TGCT	CCACTC	60
CGAACAAATCA	CTGCTGACAC	TTTCCGCAA	CTCTT	CCCGAG	TCTACT	CCAA	TTTC	CTCCGG	120	

GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	TGCAGGACAG	GGGACAGATG	AGGCAGCGGC	180
TCCCCCACC	ACGCCTCATC	TGTGACAGCC	GAGTCCTGGA	GAGGTACCTC	TTGGAGGCCA	240
AGGAGGCCGA	GAATATCACG	ACGGGCTGTG	CTGAACACTG	CAGCTTGAAT	GAGATAATC	300
ACTGTCCCAG	ACACCAAAGT	TAATTCTAT	GCTTGGAAAGA	GGATGGAGGT	CGGGCAGCAG	360
GCCGTAGAAG	TCTGGCAGGG	CTTGGCCCTG	CTGTCGGAAG	CTGTCCTGCG	GGGCCAGGCC	420
CTGTTGGTCA	ACTCTTCCC	GCCGTGGGAG	CCCTCTGCAGC	TGCATGTGGA	AAAGCCGTC	480
AGTGGCCTTC	GCAGCCTCAC	CACTCTGCTT	CGG			513

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CTGGGAGCCC	AGAAGGAAGC	CATCTCCCCT	CCAGATGCGG	CCTCAGCTGC	TCCACTCCGA	60
ACAATCACTG	CTGACACTTT	CCGAAACTC	TTCCGAGTCT	ACTCCAATTT	CCTCCGGGGA	120
AAGCTGAAGC	TGTACACAGG	GGAGGCCCTGC	AGGACAGGGG	ACAGATGAGG	CGGCAGCTCC	180
CCCCACCAACG	CCTCATCTGT	GACAGCCGAG	TCTTGGAGAG	GTACCTCTTG	GAGGCCAAGG	240
AGGCGGAGAA	TATCACGACG	GGCTGTGCTG	AAACACTGCAG	CTTGAATGAG	AATAATCACT	300
GTCAGAGACA	CCAAAGTTAA	TTTCTATGCC	TGGAAGAGGA	TGGAGGTCGG	GCAGCAGGCC	360
GTAGAAAGTCT	GGCAGGGCCT	GGCCCTGCTG	TCGGAAAGCTG	TCCTGCGGGG	CCAGGCCCTG	420
TTGGTCAACT	CTTCCCAGCC	GTGGGAGGCC	CTGCAGCTGC	ATGTGGATAA	AGCCGTCAGT	480
GGCCTTCGCA	GCCTCACAC	TCTGCTTCGG	GTC			513

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GGAGCCCCAGA	AGGAAGCCAT	CTCCCCCTCCA	GATGCGGCCT	CAGCTGCTCC	ACTCCGAACA	60
ATCACTGCTG	ACACTTTCCG	CAAACCTTC	CGAGTCTACT	CCAATTCTCT	CCGGGGAAAG	120
CTGAAGCTGT	ACACAGGGGA	GGCCTGCAGG	ACAGGGGACA	GATGAGGCAG	CGGCTCCCCC	180
CACCAACCCAT	CATCTGTGAC	AGCCGAGTC	TGGAGAGGTA	CCTCTTGGAG	GCCAAAGGAGG	240
CCGAGAAATAT	CACGACGGGC	TGTGCTGAAC	ACTGCACTGCT	GAATGAGAAAT	AATCACTGTC	300
CCGACACCA	AAGTTAATT	CTATGCTGG	AAGAGGATGG	AGGTGCGGCA	GCAGGCCGTA	360
GAAGTCTGGC	AGGGCCTGGC	CCTGCTGTG	GAAGCTGTC	TGCGGGGCCA	GGCCCTGTTG	420
GTCAACTCTT	CCCAGCCGTG	GGAGCCCCTG	CAGCTGCATG	TGGATAAAAGC	CGTCAGTGGC	480
CTTCGAGCC	TCACCACTCT	GCTTCGGGCT	CTG			513

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GCCCCAGAAGG	AAGCCATCTC	CCCTCCAGAT	GGGGCCTCAG	CTGCTCCACT	CCGAACAATC	60
ACTGCTGACA	CTTTCCGCAA	ACTCTCCGA	GTCTACTCCA	ATTTCTCCG	GGGAAAGCTG	120
AAGCTGTACA	CAGGGGAGGC	CTGAGGACAGA	GGGGACAGAT	GAGGCAGCGG	CTCCCCCCCAC	180
CACGCTCAT	CTGTGACAGC	CGAGTCTGG	AGAGGTACCT	CTTGGAGGCC	AAGGGAGGCC	240
AGAATATCAC	GACGGGCTGT	GCTGAACACT	GCAGCTTGA	TGAGAATAAT	CACTGTCCCA	300
GACACCAAAG	TTAATTCTA	TGCTTGGAA	AGGATGGAGG	TCGGGCAGCA	GGCCGTAGAA	360
GTCTGGCAGG	GCCTGGCCCT	GCTGTCGGAA	GCTGTCTGC	GGGGCCAGGC	CCTGTTGGTC	420
AACTCTTCCC	AGCCGTGGGA	GGCCCTGAG	CTGCATGTGG	ATAAAGCCGT	CGATGGCCTT	480
CGCAGCCTCA	CCACTCTGCT	TCGGGCTCTG	GGA			513

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAGAAGGAAG	CCATCTCCCC	TCCAGATGCG	GCCTCAGCTG	CTCCACTCCG	AACAATCACT	60
GCTGACACTT	TCCGCAAAC	CTTCCGAGTC	TACTCCAATT	TCCTCCGGG	AAAGCTGAAG	120
CTGTACACAG	GGGAGGCCTG	CAGGACAGGG	GACAGATGAG	GCAGCGGCTC	CCCCCACAC	180
GCCTCATCTG	TGACAGCCGA	GTCTGGAGA	GGTACCTCTT	GGAGGCCAAG	GAGGCCGAGA	240
ATATCACGAC	GGGCTGTGCT	GAACACTGCA	GCTTGAATGAA	GAATAATCAC	TGTCAGAC	300
ACCAAAGTTA	ATTTCATGCA	CTGGAAGAGG	ATGGAGGTGG	GGCAGCAGGC	CGTAGAAGTC	360
TGGCAGGGCC	TGGCCCTGCT	GTCGGAAGCT	GTCCTGCGGG	GCCAGGCCCT	GTTGGTCAAC	420
TCTTCCCAGC	CGTGGGAGCC	CCTGCAGCTG	CATGTGGATA	AAGCCGTAG	TGGCCTTCGC	480
AGCCTCACCA	CTCTGCTTCG	GGCTCTGGGA	GCC			513

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

AAGGAAGCCA	TCTCCCTCC	AGATGCGGCC	TCAGCTGCTC	CACTCCGAAC	AATCACTGCT	60
GACACTTTCC	GAAACTCTT	CCGAGTCTAC	TCCAATTCC	TCCGGGAAA	GCTGAAGCTG	120
TACACAGGGG	AGGCCTGCAG	GACAGGGGAC	AGATGAGGCC	GCAGCTCC	CCACCCACGCC	180
TCATCTGTGA	CAGGCCAGTC	CTGGAGAGGT	ACCTCTTGA	GGCCAAGGAG	GCCGAGAATA	240
TCACGACGGG	CTGTGCTGAA	CACTGCAGCT	TGAATGAGAA	TAATCACTGT	CCCAGACACC	300
AAAGTTAATT	TCTATGCCTG	GAAGAGGATG	GAGGTGCGGC	AGCAGGCCGT	AGAAGTCTGG	360
CAGGGCCTGG	CCCTGCTGTC	GGAAGCTGTC	CTGCGGGGCC	AGGCCCTGTT	GGTCAACTCT	420
TCCCAGCCGT	GGGAGCCCT	GCAGCTGCAT	GTGGATAAAG	CCGTCAGTGG	CCTTCGCAGC	480
CTCACCACTC	TGCTTCGGGC	TCTGGGAGCC	CAG			513

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAAGCCATCT	CCCCTCCAGA	TGCGGCCCTCA	GCTGCTCCAC	TCCGAACAAT	CACTGCTGAC	60
ACTTTCGGCA	AACTCTTCCG	AGTCTACTCC	AATTTCCTCC	GGGAAAGCT	GAAGCTGTAC	120
ACAGGGGAGG	CCTGAGGAG	AGGGAGACAGA	TGAGGCGGCC	GCTCCCCCA	CCACGCCCTCA	180
TCTGTGACAG	CCGAGTCTCTG	GAGAGGTACC	TCTTGGAGGC	CAAGGAGGCC	GAGAATATCA	240
CGACGGGCTG	TGCTGAACAC	TGCAGCTTGA	ATGAGAATAA	TCACTGTCCC	AGACACCAAA	300
GTAAATTCT	ATGCCTGGAA	GAGGATGGAG	GTCGGGCAGC	AGGCCGTAGA	AGTCTGGCAG	360
GGCCTGGCCC	TGCTGTCGG	AGCTGTCTG	CGGGGCCAGG	CCCTGTGTTG	CAACTCTTCC	420
CAGCCGTGGG	AGCCCCCTGCA	GCTGCATGTG	GATAAAGCCG	TCAGTGGCCT	TCGCAGCCCTC	480
ACCACTCTGC	TTCGGGCTCT	GGGAGCCCG	AAG			513

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCCATCTCCC	CTCCAGATGC	GGCCTCAGCT	GCTCCACTCC	GAACAATCAC	TGCTGACACT	60
TTCCGCAAAC	TCTTCCGAGT	CTACTCCAAT	TTCTCCGGG	GAAAGCTGAA	GCTGTACACA	120
GGGGAGGCC	GCAGGACAGG	GGACAGATGA	GGCGCGGGCT	CCCCCACCA	CGCCTCATCT	180
GTGACAGCCG	AGTCCTGGAG	AGGTACCTCT	TGGAGGCCAA	GGAGGCCAG	AATATCACGA	240
CGGGCTGTGC	TGAACACTGC	AGCTTGAATG	AGAATAATCA	CTGTCCAGA	CACCAAAGTT	300
AATTTCATG	CCTGGAAGAG	GATGGAGGTC	GGGCAGCAGG	CCGTAGAAGT	CTGGCAGGGC	360
CTGGCCCTGC	TGTCGGAAGC	TGTCCCTGCG	GGCCAGGCC	TGTTGGTCAA	CTCTTCCCAG	420
CCGTGGGAGC	CCGTCAGCT	GCATGTGGAT	AAAGCCGTCA	GTGGCCTTCG	CAGCCTCACC	480
ACTCTGCTTC	GGGCTCTGGG	AGCCCGAAG	GAA			513

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

ATCTCCCCTC	CAGATGCGGC	CTCAGCTGCT	CCACTCCGAA	CAATCACTGC	TGACACTTT	60
CGCAAACCTCT	TCCGAGTCTA	CTCCAATTTC	CTCCGGGGAA	AGCTGAAGCT	GTACACAGGG	120
GAGGGCTGCA	GGACAGGGGA	CAGATGAGGC	GGCGGCTCCC	CCCACCAACGC	CTCATCTGTG	180
ACAGCCGAGT	CCTGGAGAGG	TACCTCTTGG	AGGCCAAGGA	GGCGAGAAT	ATCACGACGG	240
GCTGTGCTGA	ACACTGCAGC	TTGAATGAGA	ATAATCACTG	TCCCAGACAC	CAAAGTTAAT	300
TTCTATGCCT	GGAAGAGGAT	GGAGGTGGG	CAGCAGGCCG	TAGAAGTCTG	GCAGGGCCTG	360
GCCCTGCTGT	CGGAAGCTGT	CCTGCCGGGC	CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	420
TGGGAGCCCC	TGCACTGCA	TGTGGATAAA	GCCGTCAGTG	GCCTTCGCAG	CCTCACCACT	480
CTGCTTCGGG	CTCTGGGAGC	CCAGAAGGAA	GCC			513

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TCCCCCTCCAG	ATGCGGCCTC	AGCTGCTCCA	CTCCGAACAA	TCACTGCTGA	CACTTTCCGC	60
AAACTCTTCC	GAGTCTACTC	CAATTCCCTC	CGGGGAAAGC	TGAAGCTGTA	CACAGGGGAG	120
GCCTGCAGGA	CAGGGGACAG	ATGAGGCAGC	GGCTCCCCC	ACCACGCC	ATCTGTGACA	180
GCCGAGTCCT	GGAGAGGTAC	CTCTGGAGG	CCAAGGAGGC	CGAGAAATATC	ACGACGGGCT	240
GTGCTGAACA	CTGCAGCTTG	AATGAGAATA	ATCACTGTCC	CAGACACCAA	AGTTAATTTC	300
TATGCCCTGGA	AGAGGATGGA	GGTCGGGCAG	CAGGCCGTAG	AAGTCTGGCA	GGGCCTGGCC	360
CTGCTGTCGG	AACTGTCCCT	GCGGGGCCAG	GCCCTGTTGG	TCAACTCTTC	CCAGCCGTGG	420
GAGCCCCCTGC	AGCTGCATGT	GGATAAAGCC	GTCAGTGGCC	TTCGCAGCCT	CACCACTCTG	480
CTTCGGGCTC	TGGGAGCCCA	GAAGGAAGCC	ATC			513

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	CGAACAAATCA	CTGCTGACAC	TTTCCGAAA	60
CTCTTCCGAG	TCTACTCCAA	TTTCCTCCGG	GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	120
TGCAGGACAG	GGGACAGATG	AGCCGGCGGC	TCCCCCCCAC	ACGCCTCATC	TGTGACAGCC	180
GAGTCCTGGA	GAGGTACCTC	TTGGAGGCCA	AGGAGGCCGA	GAATATCACG	ACGGGCTGTG	240
CTGAACACTG	CAGCTTGAAT	GAGAATAACT	ACTGTCCCAG	ACACCAAAGT	TAATTCTAT	300
GCCTGGAAGA	GGATGGAGGT	CGGGCAGCAG	GCCGTAGAAG	TCTGGCAGGG	CCTGGCCCTG	360
CTGTCGGAAG	CTGCTCTGCG	GGGCCAGGCC	CTGTTGGTCA	ACTCTCCCA	GCCGTGGGAG	420
CCCCTGCAGC	TGCATGTGGA	TAAAGCCGTC	AGTGGCCTTC	GCAGCCTCAC	CACTCTGCTT	480
CGGGCTCTGG	GAGCCCAAGAA	GGAAGCCATC	TCC			513

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CCAGATGCGG	CCTCAGCTGC	TCCACTCCGA	ACAATCACTG	CTGACACTTT	CCGCAAAC	60
TTCCGAGTCT	ACTCCAATT	CCTCCGGGAA	AAAGCTGAAGC	TGTACACAGG	GGAGGCCTGC	120

AGGACAGGGG	ACAGATGAGG	CGGC GGCTCC	CCCC ACCAACG	CCTCATCTGT	GACAGCCGAG	180
TCCTGGAGAG	GTACCTCTTG	GAGGCCAAGG	AGGCCGAGAA	TATCACGACG	GGCTGTGCTG	240
AACACTGCAG	CTTGAATGAG	AATAATCACT	GTCCCAGACA	CCAAAGTTAA	TTTCTATGCC	300
TGGAAGAGGA	TGGAGGTGCG	GCAGCAGGCC	GTAGAAGTCT	GGCAGGGCCT	GGCCCTGCTG	360
TCGGAAGCTG	TCCTGCGGGG	CCAGGCCCTG	TTGGTCAACT	CTTCCCAGCC	GTGGGAGCCC	420
CTGCA GCTGC	ATGTGGATAA	AGCCGTCAGT	GGCCTTCGCA	GCCTCACCCAC	TCTGCTTCGG	480
GCTCTGGAG	CCCAGAAGGA	AGCCATCTCC	CCT			513

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GATGCGGCCT	CAGCTGCTCC	ACTCCGAACA	ATCACTGCTG	ACACTTTCCG	CAAAC TCTTC	60
CGAGTCTACT	CCAATTCCCT	CCGGGGAAAG	CTGAAGCTGT	ACACAGGGGA	GGCTG CAGG	120
ACAGGGGACA	GATGAGGGCGG	CGGCTCCCCC	CACCACGCCT	CATCTGTGAC	AGCCGAGTCC	180
TGGAGAGGTA	CCTCTTGGAG	GCCAAGGAGG	CCGAGAATAT	CACGACGGGC	TGTGCTGAAC	240
ACTGCAGCTT	GAATGAGAAT	AATCACTGTC	CCAGACACCA	AAGTTAATTT	CTATGCCTGG	300
AAGAGGATGG	AGGTGCGGGCA	GCAGGCCGTA	GAAGTCTGGC	AGGGCCTGGC	CCTGCTGTGCG	360
GAAGCTGTCC	TGCGGGGGCCA	GGCCCTGTTG	GTCAACTTCTT	CCCAGCCGTG	GGAGCCCCCTG	420
CAGCTGCATG	TGGATAAACG	CGTCAGTGGC	CTTCGCA GGC	TCACCACTCT	GCTTCGGGCT	480
CTGGGAGCCC	AGAAGGAAGC	CATCTCCCT	CCA			513

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CGGGCCTCAG	CTGCTCCACT	CCGAACAATC	ACTGCTGACA	CTTTCCGCAA	ACTCTTCCGA	60
GTCTACTCCA	ATTCCTCCG	GGGAAAGCTG	AAGCTGTACA	CAGGGGAGGC	CTGCAGGACA	120
GGGGACAGAT	GAGGC GGGCGG	CTCCCCCAC	CACGCCTCAT	CTGTGACAGC	CGAGTCCTGG	180
AGAGGTACCT	CTTGAGGAGC	AAGGAGGCC	AGAATATCAC	GACGGGCTGT	GCTGAACACT	240
GCAGCTTGAA	TGAGAATTC	CACTGTCCA	GACACCAAAG	TTAATTCTA	TGCTTGGAAAG	300
AGGATGGAGG	TGCGGGCAGCA	GGCCGTAGAA	GTCTGGCAGG	GCCTGGCCCT	GCTGTGGAA	360
GCTGTCTGC	GGGGCCAGGC	CCTGTTGGTC	AACTCTCCC	AGCCGTGGGA	GGCCCTGCAG	420
CTGCATGTGG	ATAAAGCCGT	CAGTGGCCTT	CGCAGCCTCA	CCACTCTGCT	TCGGGCTCTG	480
GGAGCCCAGA	AGGAAGCCAT	CTCCCTCCA	GAT			513

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCCTCAGCTG	CTCCACTCCG	AAACAATCACT	GCTGACACTT	TCCGCAAAC	CTTCCGAGTC	60
TACTCCAATT	TCCTCCGGGG	AAAGCTGAAG	CTGTACACAG	GGGAGGCCTG	CAGGACAGGG	120
GACAGATGAG	GCGGCGGCTC	CCCCCACCC	GCCTCATCTG	TGACAGCCGA	GTCTGGAGA	180
GGTACCTCTT	GGAGGCCAAG	GAGGCCGAGA	ATATCACGAC	GGGCTGTGCT	GAACACTGCA	240
GCTTGAAATGA	GAATAATCAC	TGTCCCAGAC	ACCAAAGTTA	TTTCTATGC	CTGGAAGAGG	300
ATGGAGGTGCG	GGCAGCAGGC	CGTAGAAGTC	TGGCAGGGCC	TGGCCCTGCT	GTGCGAAGCT	360
GTCCTGCGGG	GCCAGGCCCT	GTTGGTCAAC	TCTTCCCAGC	CGTGGGAGCC	CCTGCAGCTG	420
CATGTGGATA	AAGCCGTCAG	TGGCCTTCG	AGCCTCACCA	CTCTGCTTCG	GGCTCTGGGA	480
GCCCAGAAGG	AAGCCATCTC	CCCTCCAGAT	GCG			513

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TCAGCTGCTC	CACTCCGAAC	AATCACTGCT	GACACTTCC	GCAAACCTTT	CCGAGTCTAC	60
TCCAATTCC	TCCGGGGAAA	GCTGAAGCTG	TACACAGGGG	AGGCCTGCAG	GACAGGGGAC	120
AGATGAGGCG	GCGGCTCCCC	CCACCACGCC	TCATCTGTGA	CAGCCGAGTC	CTGGAGAGGT	180
ACCTCTTGGA	GGCCAAGGAG	GCCGAGAATA	TCACGACGGG	CTGTGCTGAA	CACTGCAGCT	240
TGAATGAGGA	TAATCACTGT	CCCAGACACC	AAAGTTAATT	TCTATGCCCTG	GAAGAGGATG	300
GAGGTCGGGC	AGCAGGCCGT	AGAACGTCAG	CAGGGCCTGG	CCCTGCTGTC	GGAGCTGTC	360
CTGCGGGGCC	AGGCCCTGTG	GCTCAACTCT	TCCCAGCCGT	GGGAGCCCT	GCAGCTGCA	420
GTGGATAAAG	CCGTCACTGG	CCTTCGCAGC	CTCACCACTC	TGCTTCGGGC	TCTGGGAGCC	480
CAGAAGGAAG	CCATCTCCCC	TCCAGATGCG	GCC			513

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCTGCTCCAC	TCCGAACAAT	CACTGCTGAC	ACTTTCCGCA	AACTCTCCG	AGTCTACTCC	60
AATTCTCTCC	GGGGAAAGCT	GAAGCTGTAC	ACAGGGGAGG	CCTGCAGGAC	AGGGGACAGA	120
TGAGGCGGCG	GCTCCCCCCC	CCACGCTCTA	TCTGTGACAG	CCGAGTCCCTG	GAGAGGTACC	180
TCTTGGAGGC	CAAGGAGGCC	GAGAATATCA	TCACGACAC	TGCTGAACAC	TGAGCTTGA	240
ATGAGAATAA	TCACTGCTCC	AGACACAAAA	GTTAATTCT	ATGCCTGGAA	GAGGATGGAG	300
GTCGGGAGC	AGGCCGTAGA	AGTCTGGAG	GGCCTGGCC	TGCTGTCGGA	AGCTGTCTG	360
CGGGGCCAGG	CCCTGTTGGT	CAACTCTTCC	CAGCCGTGGG	AGCCCTGCA	GCTGCATGTG	420
GATAAAAGCCG	TCAGTGGCCT	TCGCAAGCCTC	ACCACTCTG	TTCGGGCTCT	GGGAGCCAG	480
AAGGAAGCCA	TCTCCCTCC	AGATGCGGCC	TCA			513

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCCACTCC	GAACAATCAC	TGCTGACACT	TTCCGAAAC	TCTTCCGAGT	CTACTCCAAT	60
TTCCCTCCGGG	AAAAGCTGAA	GCTGTACACA	GGGGAGGCC	GCAGGACAGG	GGACAGATGA	120
GGCGGCGGCT	CCCCCACCAC	CGCCTCATCT	TGACAGCCG	AGTCCTGGAG	AGGTACCTCT	180
TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	CGGGCTGTG	TGAACACTGC	AGCTTGAAATG	240
AGAATAATCA	CTGTCCCAGA	CACCAAAGTT	AATTCTATG	CCTGGAGAG	GATGGAGGTC	300
GGGCAGCAGG	CCGTAGAAGT	CTGGCAGGGC	CTGGCCCTGC	TGTCGGAAGC	TGTCCTGCGG	360
GGCCAGGCC	TGTTGGTCAA	CTCTTCCCAG	CCGTGGGAGC	CCCTGCAAGCT	GCATGTGGAT	420
AAAGCCGTCA	GTGGCCTTCG	CAGCCTCACC	ACTCTGCTTC	GGGCTCTGGG	AGCCCAGAAAG	480
GAAGCCATCT	CCCCCTCAGA	TGCGGCCTCA	GCT			513

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CCACTCCGAA	CAATCACTGC	TGACACTTTC	CGCAAACCT	TCCGAGTCTA	CTCCAATTTC	60
CTCCGGGGAA	AGCTGAAGCT	GTACACAGGG	GAGGCCTGCA	GGACAGGGGA	CAGATGAGGC	120
GGCGGCTCCC	CCCACCACGC	CTCATCTGTG	ACAGCCGAGT	CCTGGAGAGG	TACCTCTTGG	180
AGGCCAAGGA	GGCCGAGAAAT	ATCACGACGG	GCTGTGCTGA	ACACTGCAGC	TTGAATGAGA	240
ATAATCACTG	TCCCAGACAC	CAAAGTTAAT	TTCTATGCC	GGAAGAGGAT	GGAGGTGCGG	300
CAGCAGGCCG	TAGAAGTCTG	GCAGGGCCTG	GCCTGCTGT	CGGAAGCTGT	CCTGCGGGGC	360
CAGGCCCCGT	TGGTCAACTC	TTCCCAGCCG	TGGGAGCCCC	TGCAGCTGCA	TGTGGATAAA	420
GCCGTCAGTG	GCCTTCGCGAC	CCTCACCACT	CTGCTTCGGG	CTCTGGGAGC	CCAGAAGGAA	480
GCCATCTCCC	CTCCAGATGC	GGCCTCAGCT	GCT			513

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CTCCGAACAA	TCACTGCTGA	CACTTCCGC	AAACTCTTCC	GAGTCTACTC	CAATTCCTC	60
CGGGGAAAGC	TGAAGCTGTG	CACAGGGG	GCCTGCAGGA	CAGGGGACAG	ATGAGGCAGG	120
GGCTCCCCC	ACCACGCC	ATCTGTGACA	GGCGAGTCCT	GGAGAGGTAC	CTCTTGAGG	180
CCAAGGAGGC	CGAGAATATC	ACGACGGGCT	GTGCTGAACA	CTGCAGCTTG	AATGAGAATA	240
ATCACTGTCC	CAGACACCAA	AGTTAATTTC	TATGCCTGGA	AGAGGATGGA	GGTCGGGAG	300
CAGGCCGTAG	AAGTCTGGCA	GGGCCTGGCC	CTGCTGTCGG	AAGCTGTCC	GCGGGGCCAG	360
GCCCTGTTGG	TCAACTCTTC	CCAGCCGTGG	GAGCCCCTGC	AGCTGCATGT	GGATAAAAGCC	420
GTCAGTGGCC	TTCGCAGCCT	CACCACTCTG	CTTCGGGCTC	TGGGAGCCCA	GAAGGAAGGCC	480
ATCTCCCCTC	CAGATGCGGC	CTCAGCTGCT	CCA			513

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CGAACAAATCA	CTGCTGACAC	TTTCCGAAA	CTCTTCCGAG	TCTACTCCAA	TTTCCTCCGG	60
GGAAAGCTGA	AGCTGTACAC	ACGGGAGGCC	TGCAGGACAG	GGGACAGATG	AGGCAGGCC	120
TCCCCCCCAC	ACGCCTCATC	TGTGACAGCC	GAGTCCTGGA	GAGGTACCTC	TTGGAGGCCA	180
AGGAGGCCGA	GAATATCACG	ACGGGCTGTG	CTGAACACTG	CAGCTTAAT	GAGAATAATC	240
ACTGTCCCAG	ACACCAAAGT	TAATTCTAT	GCCTGGAAGA	GGATGGAGGT	CGGGCAGCAG	300
GCCGTAGAAG	TCTGGCAGGG	CCTGGCCCTG	CTGTCGGAAG	CTGTCCTGCG	GGGCCAGGCC	360
CTGTTGGTCA	ACTCTCCCA	GCCGTGGGAG	CCCCTGAGC	TGCACTGGA	TAAAGCCGTC	420
AGTGGCCCTTC	GCAGCCTCAC	CACTCTGCTT	CGGGCTCTGG	GAGCCAGAA	GGAAGCCATC	480
TCCCCCTCCAG	ATGCGGCCTC	AGCTGCTCCA	CTC			513

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACAATCACTG	CTGACACTTT	CCGAAACCTC	TTCCGAGTCT	ACTCCAATT	CCTCCGGGGA	60
AAGCTGAAGC	TGTACACAGG	GGAGGCCTGC	AGGACAGGGG	ACAGATGAGG	CGGCGGCTCC	120
CCCCACCAACG	CCTCATCTGT	GACAGCCGAG	TCCTGGAGAG	GTACCTTTG	GAGGCCAAGG	180
AGGCCGAGAA	TATCACGACG	GGCTGTGCTG	AAACACTGCAG	CTTGAATGAG	AATAATCACT	240
GTCCCAAGACA	CCAAAGTTAA	TTTCTATGCC	TGGAAGAGGA	TGGAGGTCGG	GCAGCAGGCC	300
GTAGAAAGTCT	GCGCAGGGCTC	GGCCCTGCTG	TCCGAAGCTG	TCCTGCCGGG	CCAGGCCCTG	360
TTGGTCAACT	CTTCCCAGCC	GTGGGAGGCC	CTGCAGCTGC	ATGTGGATAA	AGCCGTCACT	420
GGCCTTCGCA	GCCTCACCAAC	TCTGCTTCGG	GCTCTGGGAG	CCCAGAAGGA	AGCCATCTCC	480
CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	CGA			513

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GCCCCACCAAC	GCCTCATCTG	TGACAGCCGA	GTCCCTGGAGA	GGTACCTCTT	GGAGGCCAAG	60
GAGGCCGAGA	ATATCACGAC	GGGCTGTGCT	GAACACTGCA	GCTTGAATGA	GAATATCACT	120

GTCCCAGACA	CCAAAGTTAA	TTTCTATGCC	TGGAAGAGGA	TGGAGGTCGG	GCAGCAGGCC	180
GTAGAAGTCT	GGCAGGGCCT	GGCCCTGCTG	TCGGAAGCTG	TCCTGCAGGGG	CCAGGCCCTG	240
TTGGTCAACT	CTTCCCAGCC	GTGGGAGCCC	CTGCAGCTGC	ATGTGGATAA	AGCCGTCAGT	300
GGCCTTCGCA	GCCTCACCA	TCTGCTTCGG	GCTCTGGGAG	CCCAGAAGGA	AGCCATCTCC	360
CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	CGAACAAATCA	CTGCTGACAC	TTTCCGCAAA	420
CTCTTCCGAG	TCTACTCCAA	TTTCCTCCGG	GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	480
TGCAGGACAG	GGGACAGATG	A				501

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu
1				5				10			15				
Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His
					20			25			30				
Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe
					35			40			45				
Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp
					50			55			60				
Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu
					65			70			75			80	
Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp
						85			90			95			
Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu
					100			105			110				
Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala
					115			120			125				
Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val
					130			135			140				
Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala
					145			150			155			160	
Cys	Arg	Thr	Gly	Asp	Arg										
					165										

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu
1					5			10			15				
Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser
					20			25			30				
Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro
					35			40			45				
Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg
					50			55			60				
Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile
					65			70			75			80	
Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala
					85			90			95				
Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly
					100			105			110				
Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly
					115			120			125				
Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu
					130			135			140				
Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys
					145			150			155			160	
Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile						
					165			170							

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gly Gly Gly Ser
1

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Gly Gly Gly Ser Gly Gly Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Ser Gly Gly Ser Gly Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Glu Phe Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Glu Phe Gly Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Glu Phe Gly Gly Asn Gly Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Gly Gly Ser Asp Met Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCGCGCCCAT GGACAATCAC TGCTGAC

27

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

TCTGTCCCCCT GTCCT

15

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCGCGCAAGC TTATTATCGG AGTGGAGCAG CTGAGGCCGC ATC

43

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GCCCCACCAAC GCCTCATCTG T

21

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